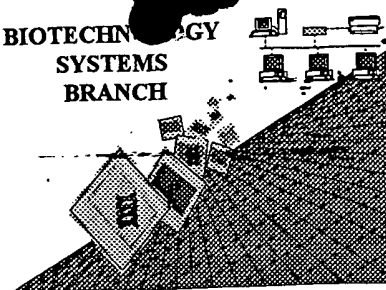


Shubert

BIOTECHNOLOGY
SYSTEMS
BRANCH



#13
Linda
8/18/00

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/101,423

Source: 1632

Date Processed by STIC: 8/9/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/101,423

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes space.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) 2 are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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R. Shukla

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1632

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
 TIME: 14:53:45
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error throughout.

Input Set : A:\ES.txt
 Output Set: N:\CRF3\08092000\I101423.raw

Does Not Comply
 Corrected Diskette Needed

see item 5
 on Error summary
 sheet

3 <110> APPLICANT: Rudland, Philip S.
 4 Barraclough, Roger B.
 W--> 5 <120> TITLE OF INVENTION: Metastasis Inducing DNA=s
 W--> 6 <130> FILE REFERENCE: WPT 0114 PUS
 W--> 7 <140> CURRENT APPLICATION NUMBER: US 09/101,423
 8 <141> CURRENT FILING DATE: 1998-11-27
 9 <150> PRIOR APPLICATION NUMBER: PCT/GB97/00074
 10 <151> PRIOR FILING DATE: 1997-01-10
 W--> 11 <160> NUMBER OF SEQ ID: 6

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1033 base pairs
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 18 <400> SEQUENCE: 1
 E--> 19 cttccttggt gctctatgtc ttgcctctcc cttctccag tcccatatag
 20 ccataacccat 60
 E--> 22 cttgacagac tctgggacag tcccctctgc tctcctgttg gcgcctgagt
 23 cccctttttgc 120
 E--> 25 ctgaggaccc ttcacgtagc ctcccatctg gatgacctag tagaagacgt
 26 gggaagtgtt 180
 E--> 28 cacactcagg taactgagca gagctcagag atttaaagtg agtctgggga
 29 gctcagagga 240
 E--> 32 ttgatctgct gccttaaaaa gccaatgga tgactaacc agactattgt
 33 cacttttaggt 300
 E--> 35 gggaagtcac tagcatatct gatgggtcac atctgagaaa ggtttctagc
 36 agtgggtggcc 360
 E--> 38 ttgtgtgagc agcatggcgt gtatcatggt gtgcagcata ctgagctgct
 39 ttgcaacct 420
 E--> 41 cgaggctctt cttcagtatt aggggaacca ctggtgttga acatggtcca
 42 agaatacagt 480
 E--> 44 catgtgagga gaatcccaat gcgtcaggag aaaacgagag tctgtgacct
 45 ccattcttca 540
 E--> 47 agatacagaa ttattcttgg actgtgtttt catgctcctt gtggatggga
 48 gtgagtttac 600
 E--> 50 ttcagggttaa tcagcattgc ttactgttgg tattcaagta aatgcttaaa
 51 ttatcctgga 660
 E--> 53 tatacctctg tgggaagcag gtttttgata catgcagett gtccttgtga
 54 ttgatactgc 720
 E--> 56 ttgaactcaa gagaactttg ctcatgtgat ctttcttaac cgatggagta
 57 gaaactgtct 780
 E--> 59 gatgctctca ataaagtgg ctcttgcaag agacgttagt ctgtcctgtt
 60 tatctgctcc 840
 E--> 63 attcttccgc tcccacggcc tctacagcac taaaccaccc accgatagac

format error

see item 1 on Error
 summary sheet

Please ensure
 all bases are in
 lower-case letters,
 per new sequence
 Rules format.

The CRF program
 converted letters to
 lower-case.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

64 tcagtccttc 900
E--> 66 actgacaaac atcaccagag gctcttaact gagattataa actgttacta
67 gatgatgggt 960
E--> 69 ggaatcgctc cccagaaaca taaacattta cttggagaac tcaagacccc
70 tttgtagaca 1020
72 taactcccat ggt
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 1058 base pairs
76 <212> TYPE: DNA
W--> 78 <213> ORGANISM: *mandatory name* identifier and response
78 <400> SEQUENCE: 2
E--> 79 attgctgtga gcctatttagc gacatttggt gacgccctt ttaagggggt
80 agatacaaa 60
E--> 82 aatgggttga aattctgtgc cacaacgct ctccatgttt tcacaattac
83 acttgcaacc 120
E--> 85 tgtggtcagc agccagaatt tagggatgtg atgggacagg gtcggggaaa
86 gaaggagaa 180
E--> 88 ggtaaaggaa agacagcagc ttaaagtcca aacagctcca ggagactac
89 tgtagaaata 240
E--> 91 acatcagacc atgaggagaa ttgatcatcat tgtttttcaa tgggtatcgc
92 caagggaact 300
E--> 95 ttccatctga ttaaaaaata ttactgctgg cactaaatcc aattggaaat
96 gccccacaca 360
E--> 98 atttatcttc cacttcatgc tgetaccata tgctgacgt ggcggagcag
99 aagcattccc 420
E--> 101 tccggttctg ataaatagta ctttgtaaat atttgagac gggagctctg
102 gtgacaggga 480
E--> 104 acacgtacaa accggcctgt ttatcatgtt cccgatagag gccctcttgc
105 acgtacagga 540
E--> 107 ccccaaaaaca gtcaggatgc tgtgaatttc cttccatgaa gccttgttca
108 caattagcaa 600
E--> 110 ccattggagg aagcaggctg cactgtctac cacaagtggc actttccaaa
111 gagcacacat 660
E--> 113 atattggagc aagacatttt gctggctgac tgggtgctgtg taagctgata
114 aactgctata 720
E--> 116 tttattaaac tggcttttct ttgaacaccc cactcaagga aaaaaaaca
117 cacttagggt 780
E--> 119 gacattattt ggagatgaag tctttataga gatgcttaag tttaaacgag
120 actttttaaag 840
E--> 122 ccggctctat tccatttaat gaatgggtgc cctacaaagg aagaaactgg
123 gacagaggta 900
E--> 126 tgtacacttg tgtgtgtgtg agagacaacg tgaggagctg aagaggagca
127 cgtacaagtc 960
E--> 129 agagaaaggc tgacccttat tcacactgag caaacagtc atgtgtgggt
130 cgatagatga 1020
132 gagtatcccc caagactcac acattcgaac gcttggtc
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 1008 base pairs
136 <212> TYPE: DNA

1033

same error
(see items 11 and 12 on Error Summary Sheet)

same format error

1058

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

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137 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 3
E--> 140 aggaccagag ttcacatccc atcaaatggc ccagaagggt ttaatgctgt
141 cttttggccc 60
E--> 143 agggggcgaac tgcacacaca tgtgcacata cacttacaga gacacacatt
144 cagcagcata 120
E--> 146 agaacacaat cacaaataaa aaaaatottg aaaaatttta agctaaaatt
147 gtttaagaaat 180
E--> 149 aacatatata caattttttt ttattttttt aaagatttat ttatttaattg
150 tatatgagta 240
E--> 152 cactgctctt cctccagac atagcagtag agggcatcgg atccattac
153 agatgggtgt 300
E--> 155 gagccaccat gtggtttcac agatgggtgt gagccaccat gtggtttcac
156 gaattgaact 360
E--> 158 caggacccttt ggaagagcag tcagtgtctt taacctctaa gccatctctc
159 ctgaccctta 420
E--> 161 tatacaattt taatgctacg tacacacaac ttctctttcc tttaatgggt
162 gagatttttg 480
E--> 164 tctggagaag taagaataaa ggagggaag aacattgctt tcacattgca
165 ccagtgggaa 540
E--> 167 cagcgtgttt aaagtaggaa tgccatgaaa tgactggcct gccttctcat
168 tactgttctt 600
E--> 170 cccactcctc cttttaactg gagctccttt atctaattta ttagtttgac
171 gatacccagg 660
E--> 173 gttttctctt gttttgatct ttttaagaca gagactcacc atatagccct
174 ggctggcctg 720
E--> 176 aagctcacta tgtagaccag tctggccttg aactcaaagg agatctatct
177 gcttctagt 780
E--> 179 gctgggatta aaggtctgtg ctaccaagtc tggcttgagg ctttggagca
180 gcctcgggtt 840
E--> 182 tggccttctt taaggatctc taagtagca gtaagtagcc tagccatgct
183 gttgtaggaa 900
E--> 185 gttgttctgt catcctggct ccagcacaaa ggcagtcact aaacgtcggc
186 ctcatttcat 960
E--> 189 cagagctgaa tgcaaatcc ttgtgtctct cctgtgtcct cctggaac
E--> 190 1008
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 1088 base pairs
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 4
E--> 198 agttggggac acagcttget tgattaagat gtttcttggg aaaaggaggt
199 aagcetaatg 60
E--> 201 atttccaatg gaaaggactg ctaattgggg aggcaatggt gcttaattgg
202 gacacctgcy 120
E--> 204 ggtaattaaa agctctctcc cagtggcctt tctgttttt ggctctggga
205 ggcgaaggca 180
E--> 207 ttgagaggga tgcaggcatt ctaagggtg gttcttggtt tctccttcc
208 cctctgtcca 240

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

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E--> 210 aactcagtga ggtatccctg tctgtgctgt ccttagagtg ccgtcctgag
211 gccttggtga 300
E--> 213 gttaaggctct ctggatctga gctgcctcag ggaaacgcag gagctcattg
214 gaaaggggag 360
E--> 216 aaccaggcaa aggtgttggc tgtgacctca gaattctgag gggcaaaggt
217 tcaaggctaa 420
E--> 220 ctctcattat agagcaagtt tgagactggc ctgggaacaa aaatataaag
221 tgagtgaagt 480
E--> 223 catatgacag cacctgagga gtcctgtccc tagagatcat aaggacctgg
224 ctgctgggga 540
E--> 226 cttgttgacag atggcacttt gtgtcgagag aggggacctg cccagcatg
227 ggaggccctg 600
E--> 229 gaagatccctc tggattaact gtgaacactg attgctgctt tataacctgga
230 gttgtgctgt 660
E--> 232 tatctggtac acatctgctg ggtgaatgag ttcattggct ttatttcagt
233 gaggtattta 720
E--> 235 cctgaggaga aagaaggact ggtgccacaa agcacagctt ttaaatctgt
236 ggggtgtgac 780
E--> 238 ccattatgga ctatcataac tgagtgcagg tatcaagaat actttagcag
239 gtggtaaaaa 840
E--> 241 gatttttgaa tgcgcaacga ccaaaactga actcaaaaaa caagcatggc
242 atggatcctg 900
E--> 244 ggtgtcctcg gaagcacttg cctttactgc attgtgcgac ttgacggtag
245 ccttggttct 960
E--> 247 gaatgcacaa cacgtgggct ttgggtgca caggccacca cgccgtgcct
248 gaaacacctc 1020
E--> 251 agctcaggtt tgtgctatg tectatgact tggacttact tttattgcac
252 atataaatat 1080
254 tttcctgc 1088
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 960 base pairs
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 5
E--> 263 gagggggtgg tggcacagtt atgtttttgt aggaagggtt ccatgaacct
264 cagcagagct 60
E--> 266 cgggttagaa atttaaaagc cctgagggga attttttttt taaatcgcta
267 tgaatctgac 120
E--> 269 atgagaaaaa cagatcagaa acgttcttgt gcttcagaaa aggacaagtg
270 tgtgagctaa 180
E--> 272 cagactgcac actggtgttc gaggcacatc tggatcacag gagcgtcaga
273 taatgtcccc 240
E--> 275 aaaggtaaat gcatttgctt gcacagtacc gagtgtgggtg ggggggtgcct
276 acagcccagc 300
E--> 278 ggttctcaac ettcctgatg ettcgacctt ttaatacagt gcctcatgct
279 ctggtgacct 360
E--> 281 ccccaacctt aaaattattt ttgttctgt tcataactgt gattttgata
282 ctgttatgaa 420
E--> 284 ttgtaatatata aataattttg aagaaagagg ttgccaagg gtttgagaac

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

```

      285 tgctgttcta      480
E--> 287 gccccacgtg gatggttttt cgtcatttgg ggtttttatg aggcagagtc
      288 ttatgtagcc      540
E--> 290 caggctagca gcctagaatg tgctacttag ctgaggaata accttggaac
      291 ttctgaggac      600
E--> 293 tggagagact ggcttagtcc tcaagaaact ggaaatagct ggagtttggc
      294 tacttgtggg      660
E--> 296 ttctttttt ttcaaaccct ttctactcct ttccaccct gtcggccccc
      297 taacactaaa      720
E--> 299 taagaaagag aaaggggagc atagagggga aaagaaaccc ctgaataacg
      300 tcagtagttg      780
E--> 302 gcaaaggggg gtgacatatg ttgtcattag accacatcct ggtgattaag
      303 gggagtgcaag      840
E--> 305 ttccctgggg caagtttgat ctttctgtga acgatatacta atttcttctc
      306 cctgttgctt      900
E--> 308 cgtctttgtg aacaacgact tgataaccca caatggacca tcaaccaaac
      309 aaccaaccat      960
      311 <210> SEQ ID NO: 6
      312 <211> LENGTH: 1090 base pairs
      313 <212> TYPE: DNA
      314 <213> ORGANISM: Homo sapiens
      316 <400> SEQUENCE: 6
E--> 317 ttgtctctgg tgttacttgt ttcccatctt ctgacagtgg ttgaccttc
      318 tatacgctcg      60
E--> 320 tgtgtcagga gtgctgtaga cctattttcc tgttttcttt cagccagtta
      321 caggaacaga      120
E--> 323 gtgttctact gtcagatgtg tagctgttcc tgtccactga ctttcaagct
      324 gtctctgtgt      180
E--> 326 gcaggaacca gaagggcctg tccctacttc tactgggccc ctacgcacag
      327 ggggcctaga      240
E--> 329 tgggtctagg tgttttcttc tagagcctga aatgtgggca gagagttagc
      330 tcctctgggt      300
E--> 332 tcctaggtat gtcttccctc ctgaagggtc agctctccct tccatgggat
      333 atgggtgcag      360
E--> 335 ggagctgttt gaccaggtcc tctcaaatcc ggggtgcagtc tggaccgcag
      336 gctcctgtag      420
E--> 338 cttgcctgct gcaatcttcc cgcaccaga ggcaccaag ttctctctt
      339 ggccaaggat      480
E--> 341 gtgggcaaaag gtgggcagaa gtggcaatct ctctgcctc agcgtctcag
      342 gattgcctc      540
E--> 344 acttctgggc aatccgctct ctctccaca gggtttggga gcagggagct
      345 gtgggccggg      600
E--> 348 atcaggcaaaa ggtttgaggc aaccagttag aaactggaag tgtcaggtcc
      349 cagaggaatt      660
E--> 351 ttgcctttgt gtgtcctgag tccaccaggc aggtcacttg gagcagaaaa
      352 attggttttc      720
E--> 354 cctcgggtct caggcctgaa gttgcacctc agggttggct ttcagctgta
      355 cctgtggaaa      780
E--> 357 gtatggtttt aaaaatctaa gatagctatc atgcagcaag gcttgtgtaa

```

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/101,423

DATE: 08/09/2000
TIME: 14:53:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\08092000\I101423.raw

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358 aatgtctatt 840
E--> 360 tggttcccttt atgacttact tttgtgtac tgaggatcaa acctagggtc
361 tcaagcagtc 900
E--> 363 atcacaattc tctgtcactg atccagctcc atttctatct tcttttgtcc
364 cgcgcgatct 960
E--> 366 ctgcgccagca agaaaacacg ctaggggacat acgaatcctt gctgcagcca
367 aaacttttat 1020
E--> 369 tgaatcttaa ggagaagccc gcgcaccgga ctggcgcggt ttatatacac
370 cctagcacag 1080
372 tgcattccaca 1090
W--> 374 N:\clients\W\WPT\0114pusa\sequence list with pg #s.wpd
E--> 375 sandy m. 7-21-00
E--> 376 shelly 07/24/00
E--> 378 -14-

same

delete at end of file

VERIFICATION SUMMARY

DATE: 08/09/2000

PATENT APPLICATION: US/09/101,423

TIME: 14:53:46

Input Set : A:\ES.txt

Output Set: N:\CRF3\08092000\I101423.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
 L:6 M:283 W: Missing Blank Line separator, <130> field identifier
 L:7 M:283 W: Missing Blank Line separator, <140> field identifier
 L:11 M:283 W: Missing Blank Line separator, <160> field identifier
 L:19 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
 L:19 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=1
 M:254 Repeated in SeqNo=1
 L:78 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:79 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:2
 M:112 Repeated in SeqNo=2
 M:254 Repeated in SeqNo=2
 L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
 M:112 Repeated in SeqNo=3
 M:254 Repeated in SeqNo=3
 L:198 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:4
 M:112 Repeated in SeqNo=4
 M:254 Repeated in SeqNo=4
 L:263 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:5
 M:112 Repeated in SeqNo=5
 M:254 Repeated in SeqNo=5
 L:317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:6
 M:112 Repeated in SeqNo=6
 M:254 Repeated in SeqNo=6
 L:374 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
 L:375 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
 L:375 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
 L:375 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
 L:375 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
 L:375 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
 L:375 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:376 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
 L:378 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1090 Found:1107 SEQ:6

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 AUG 18 2000
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